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| Helix Systems -- Center for Information Technology |

| http://helix.nih.gov |

| National Institutes of Health, Department of Health and Human Services |

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| DNAWorks Web Site: http://helixweb.nih.gov/dnaworks |

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| Send all correspondence to webtools@helix.nih.gov |

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Job started on 10/02/2011 at 19:39:44

Job name: ME100211sbPSTP

Output will be sent to maeaston25@gmail.com

Starting 1 trial...

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PARAMETERS FOR TRIAL 1

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Total Size Of Gene ......... 723 nt

Protein Residues ........... 241

Mutatable Residues ......... 235

Fixed Nucleotides .......... 18 nt

Oligo Size ................. 60 nt

Annealing Temp ............. 62 +/- 1\*C

Oligo Concentration ........ 1.00E-7 M

Sodium Concentration ....... 5.00E-2 M

Mg2+ Concentration ......... 2.00E-3 M

Codon Frequency Threshold .. 10%

Repeat Threshold ........... 8 nt

Mispriming Threshold ....... 8/18 (6 exact) nt

100 optimization rounds, best = 3.436 Rep = 6 Mis = 0

The total codon usage score ........... 0.000

The total length score ................ 0.000

The total melting temperature score ... 0.000

The total repeat score ................ 0.000

The total pattern score ............... 0.000

The total mispriming score ............ 0.000

The total AT content score ............ 0.000

The total GC content score ............ 0.000

The total fixed gap score ............. N/A

The OVERALL score ...... 0.000

Finished trial 1 : rate = 0.2 min/cyc : time remaining = 0.0 min.

FINAL SUMMARY FOR 1 SOLUTION

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# Tm Len | Score TmRange Short Long #Olig #Repeat #Misprime

1 62 60 | 0.000 1.8 15 60 18 0 0

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Finished